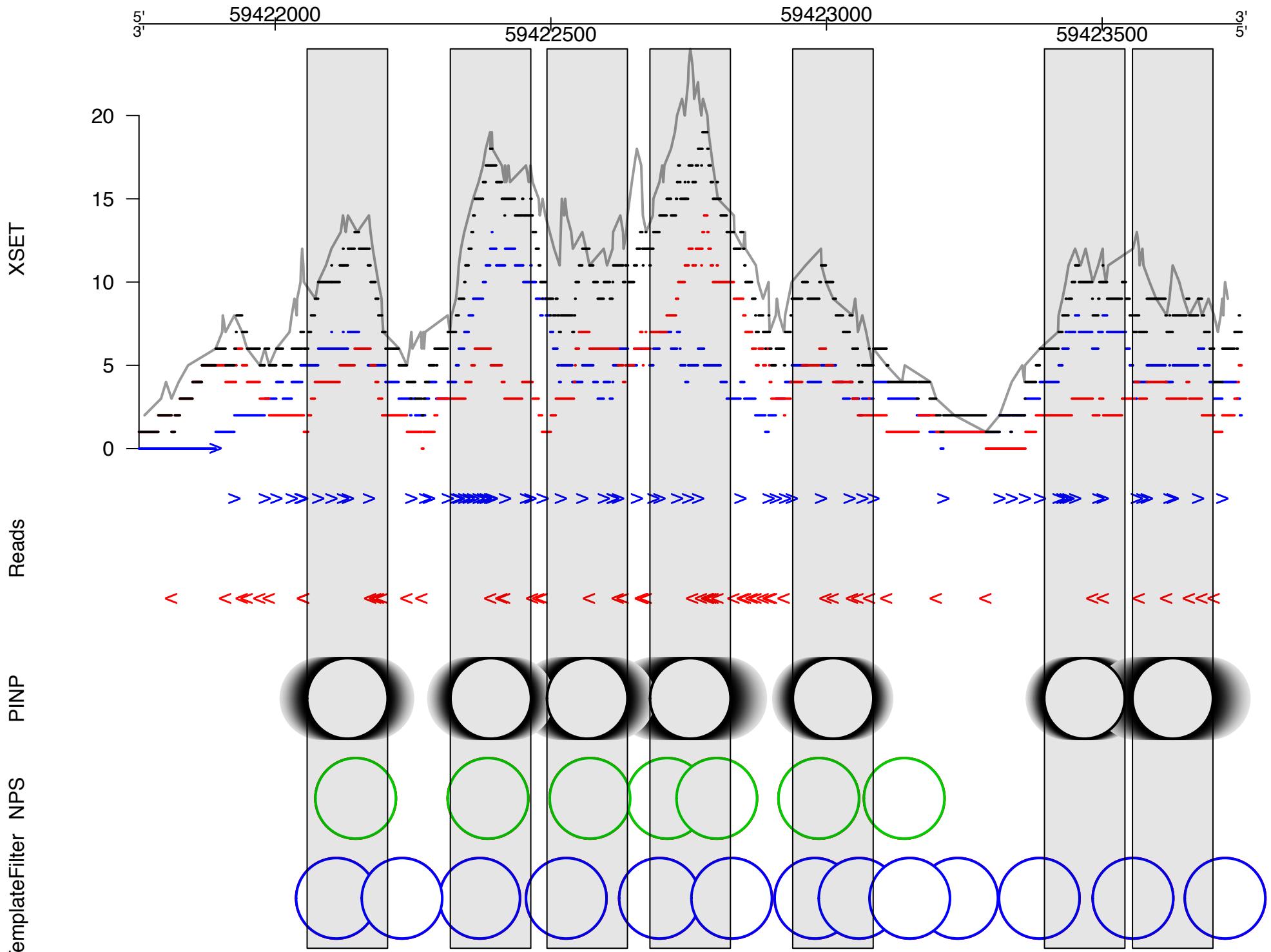


Examples of raw aligned reads and predicted nucleosomes

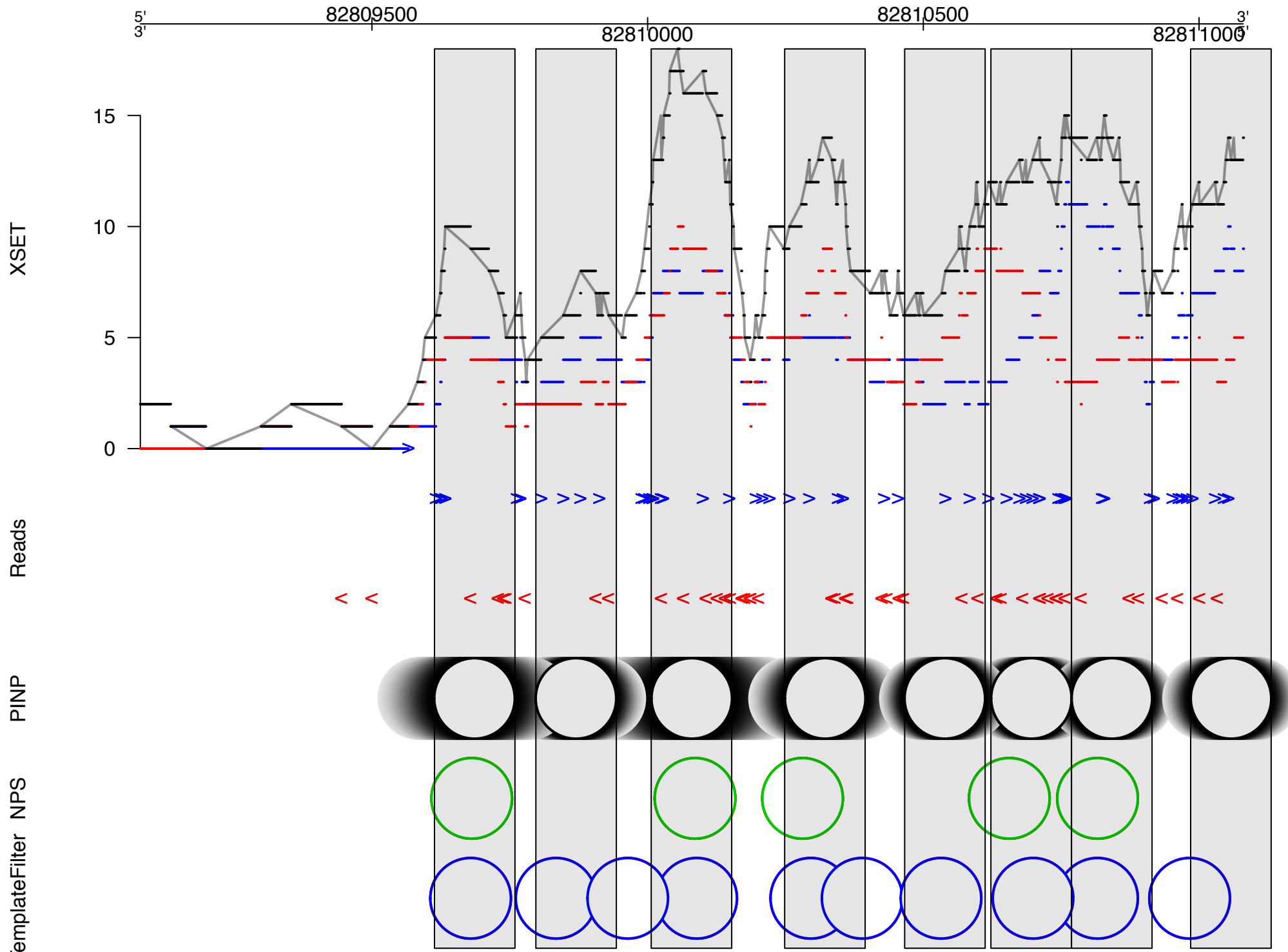
The figures in this file show examples of nucleosomes predicted using PING, NPS, and TemplateFilter in 2kb genomic regions from three different real data sets. Page 2 and 3 are generated from Hoffman's mouse sonicated ChIP-seq data. Page 4 and 5 are generated from Heinz's mouse sonicated ChIP-seq data. Page 6 and 7 are generated from Kaplan's yeast MNase-seq data.

Blue arrowheads represent aligned forward-strand reads; red show aligned reverse-strand reads. The curves shown above the reads are XSET profiles (blue for forward reads, red for reverse reads, black and gray considering all reads). The extension length for blue, red and black XSET profiles is the median of estimated δ 's in the region, whereas the extension length of gray profile is fixed at 147 bp. The circles are predicted nucleosomes for (top to bottom) PING, NPS and TemplateFilter. The grayscale smears for PING predictions represent uncertainties for predicted nucleosome locations.

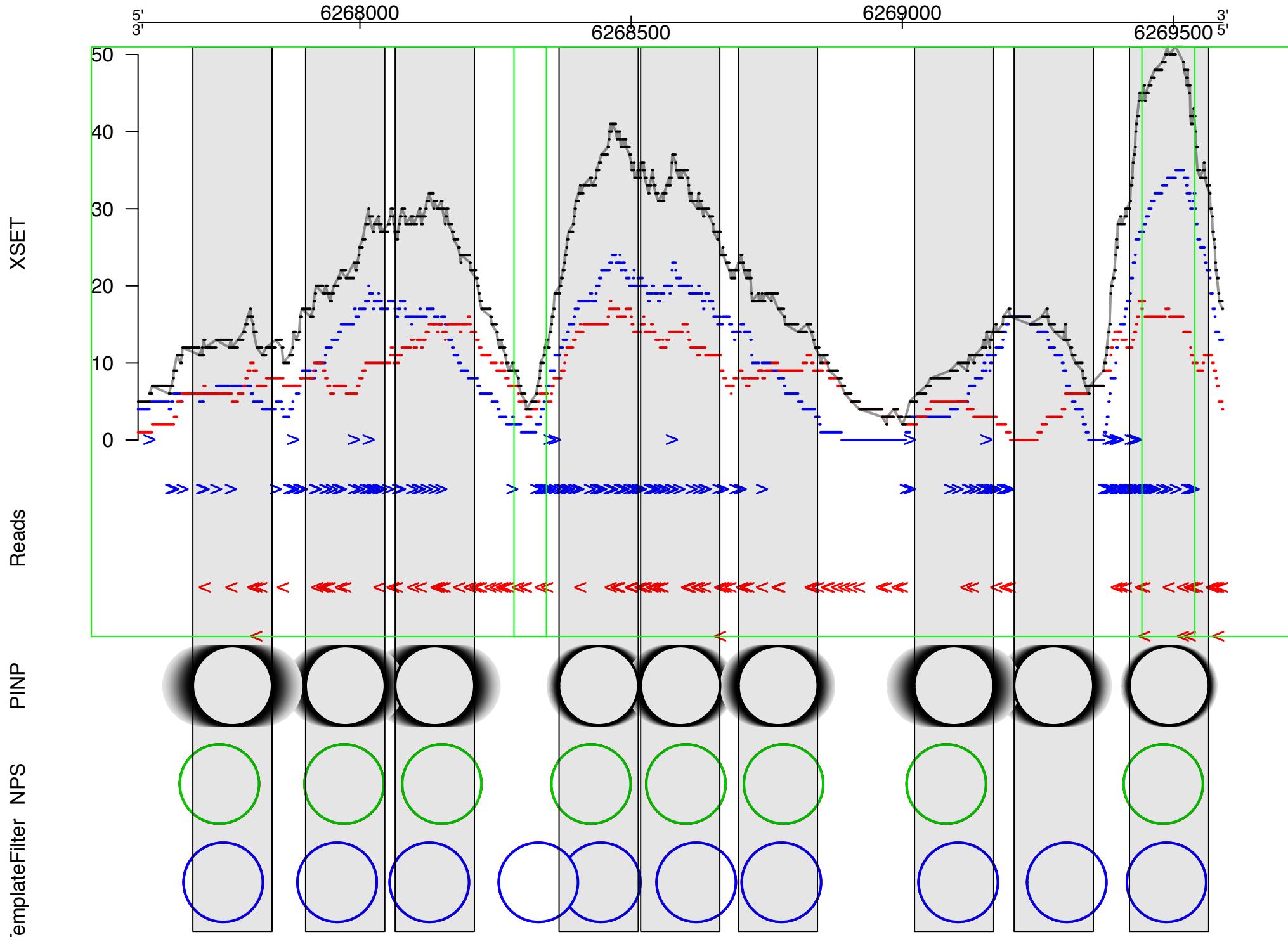
Brad, chr10:59421753–59423753(2000bps), XSET extend 122 bps



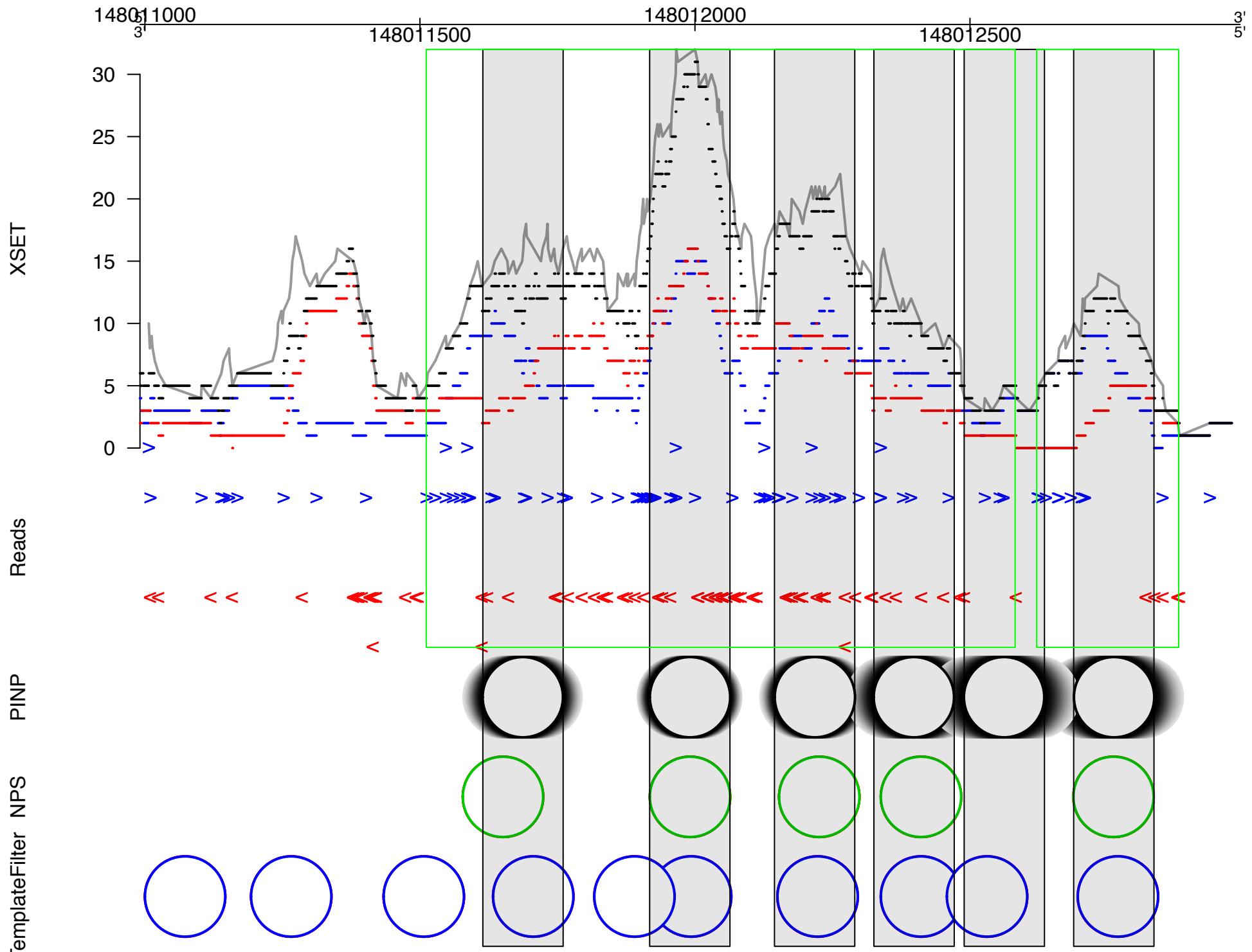
Brad, chr12:82809080–82811080(2000bps), XSET extend 146 bps



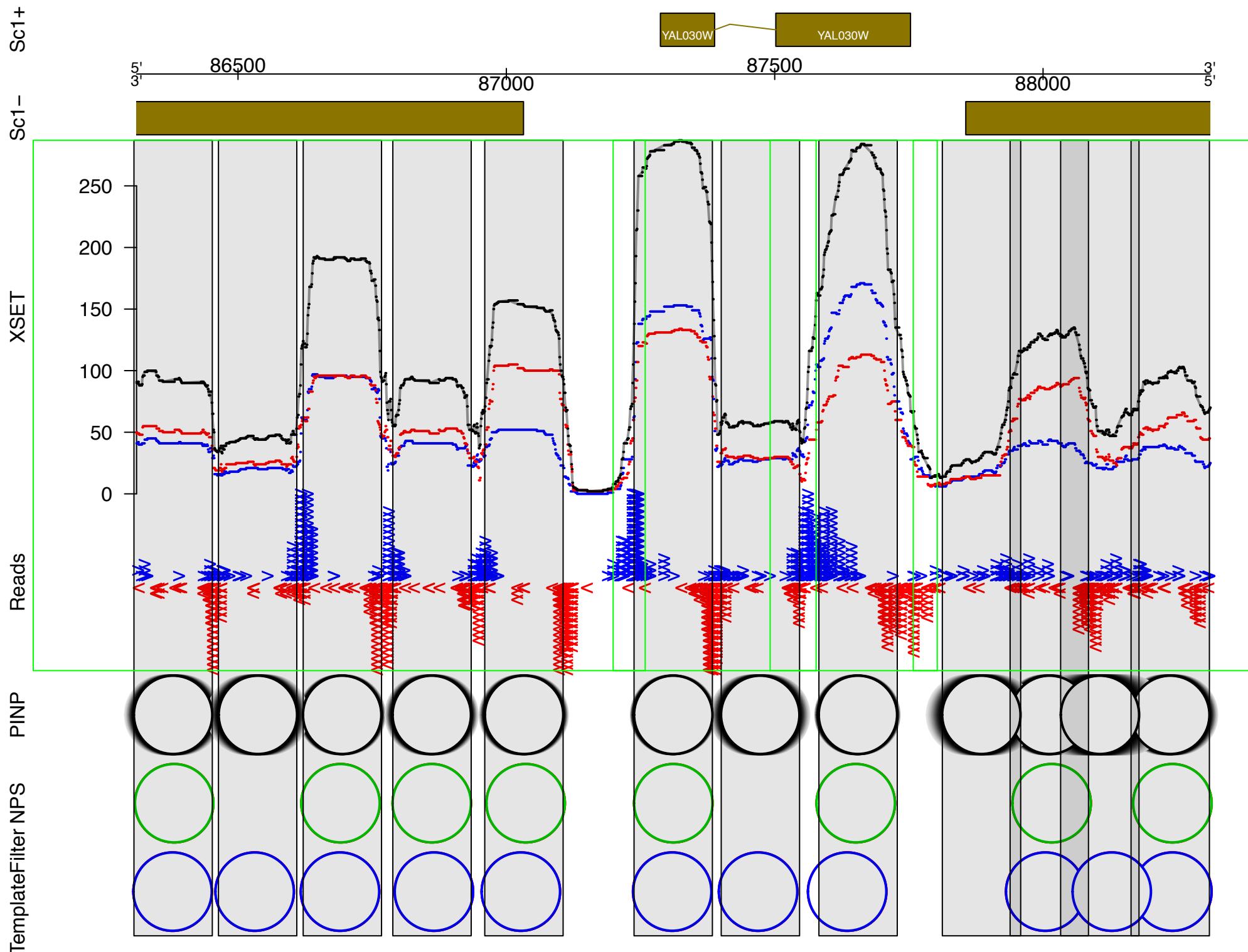
Heinz, chr19:6267591–6269591(2000bps), XSET extend 147 bps



Heinz, chr5:148010991–148012991(2000bps), XSET extend 126 bps



GSM351492_YPD_NOCL_R4, chr1:86311–88311(2000bps), XSET extend 147 bps



GSM351492_YPD_NOCL_R4, chr9:410055–412055(2000bps), XSET extend 150 bps

